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SEQUENCE LISTING

<110> M&E Biotech A/S  
STEINAA, Lucilla  
NIELSEN, Klaus Gregorius  
DALUM, Iben  
HAANING, Jesper  
LEACH, Dana  
BIRK, Peter  
MOURITSEN, Soren  
GAUTAM, Anand  
KARLSSON, Gunilla

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<120> NOVEL METHODS FOR THERAPEUTIC VACCINATION

<130> 22113 PC 1

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<160> 33

<170> PatentIn Ver. 2.1

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<212> DNA

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<223> Human PSM'

<220>

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<222> (4)..(6)

<223> ggt or tgg encoding Gly and Trp, respectively

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Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe  
20 25 30

ttt ctc ctc ggc ttc ctc ttc ggg tgg ttt ata aaa tcc tcc aat gaa 144  
Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu  
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Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu  
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Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile  
65 70 75 80

cca cat tta gca gga aca gaa caa aac ttt cag ctt gca aag caa att 288  
Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile  
85 90 95

caa tcc cag tgg aaa gaa ttt ggc ctg gat tct gtt gag cta gca cat 336  
Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His  
100 105 110

tat gat gtc ctg ttg tcc tac cca aat aag act cat ccc aac tac atc 384  
Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile  
115 120 125

tca ata att aat gaa gat gga aat gag att ttc aac aca tca tta ttt 432  
Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe  
130 135 140

gaa cca cct cct cca gga tat gaa aat gtt tcg gat att gta cca cct 480  
Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro  
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Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met	
180 185 190	
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Lys Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val	
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Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly	
210 215 220	
gtc att ctc tac tcc gac cct gct gac tac ttt gct cct ggg gtg aag	720
Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys	
225 230 235 240	
tcc tat cca gat ggt tgg aat ctt cct gga ggt ggt gtc cag cgt gga	768
Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg Gly	
245 250 255	
aat atc cta aat ctg aat ggt gca gga gac cct ctc aca cca ggt tac	816
Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr	
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cca gca aat gaa tat gct tat agg cgt gga att gca gag gct gtt ggt	864
Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly	
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Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr Asp Ala Gln Lys	
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Gly Ser Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn	

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Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu  
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Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile

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Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile  
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Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His  
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Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile  
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Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe  
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Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro  
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Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr  
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Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly  
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Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr Asp Ala Gln Lys

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Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg  
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Gly Ser Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn  
325 330 335

Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val  
340 345 350

Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro  
355 360 365

Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly  
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Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Ile Val Arg  
385 390 395 400

Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile  
405 410 415

Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr  
420 425 430

Glu Trp Ala Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala  
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Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val  
450 455 460

Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu  
465 470 475 480

Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu Ser  
485 490 495

Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro Arg Ile  
500 505 510

Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe Gln Arg Leu

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Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu  
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Leu Val Glu Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val  
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Ala Gln Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val  
580 585 590

Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala  
595 600 605

Asp Lys Ile Tyr Ser Ile Ser Met Lys His Pro Gln Glu Met Lys Thr  
610 615 620

Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr  
625 630 635 640

Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser  
645 650 655

Asn Pro Ile Val Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu  
660 665 670

Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg  
675 680 685

His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser  
690 695 700

Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp  
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Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala  
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Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala

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 -5 -1 1 5  
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 Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His  
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 Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr  
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 Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val  
 45 50 55  
 cag ggc tac gtg ctc atc gct cac aac caa gtg agg cag gtc cca ctg 288  
 Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu  
 60 65 70  
 cag agg ctg cgg att gtg cga ggc acc cag ctc ttt gag gac aac tat 336  
 Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr  
 75 80 85

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gtc aca ggg gcc tcc cca gga ggc ctg cgg gag ctg cag ctt cga agc 432  
 Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser  
 110 115 120

ctc aca gag atc ttg aaa gga ggg gtc ttg atc cag cgg aac ccc cag 480  
 Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln  
 125 130 135

ctc tgc tac cag gac acg att ttg tgg aag gac atc ttc cac aag aac 528  
 Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn  
 140 145 150

aac cag ctg gct ctc aca ctg ata gac acc aac cgc tct cgg gcc tgc 576  
 Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys  
 155 160 165

cac ccc tgt tct ccg atg tgt aag ggc tcc cgc tgc tgg gga gag agt 624  
 His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser  
 170 175 180 185

tct gag gat tgt cag agc ctg acg cgc act gtc tgt gcc ggt ggc tgt 672  
 Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys  
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gcc cgc tgc aag ggg cca ctg ccc act gac tgc tgc cat gag cag tgt 720  
 Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys  
 205 210 215

gct gcc ggc tgc acg ggc ccc aag cac tct gac tgc ctg gcc tgc ctc 768  
 Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu  
 220 225 230

cac ttc aac cac agt ggc atc tgt gag ctg cac tgc cca gcc ctg gtc 816  
 His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val  
 235 240 245

acc tac aac aca gac acg ttt gag tcc atg ccc aat ccc gag ggc cgg 864  
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Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln				
285	290	295		
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Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys				
300	305	310		
ccc tgt gcc cga gtg tgc tat ggt ctg ggc atg gag cac ttg cga gag				1056
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315	320	325		
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aag atc ttt ggg agc ctg gca ttt ctg ccg gag agc ttt gat ggg gac				1152
Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp				
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Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe				
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Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro				
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Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu				
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430 435 440

ctg gcc ctc atc cac cat aac acc cac ctc tgc ttc gtg cac acg gtg 1440  
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ccc tgg gac cag ctc ttt cgg aac ccg cac caa gct ctg ctc cac act 1488  
Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr  
460 465 470

gcc aac cgg cca gag gac gag tgt gtg ggc gag ggc ctg gcc tgc cac 1536  
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475 480 485

cag ctg tgc gcc cga ggg cac tgc tgg ggt cca ggg ccc acc cag tgt 1584  
Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys  
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Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu  
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Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg  
650 655 660 665

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670 675 680

gcg atg ccc aac cag gcg cag atg cgg atc ctg aaa gag acg gag ctg 2160  
Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu  
685 690 695

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Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys  
700 705 710

ggc atc tgg atc cct gat ggg gag aat gtg aaa att cca gtg gcc atc 2256  
Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile  
715 720 725

aaa gtg ttg agg gaa aac aca tcc ccc aaa gcc aac aaa gaa atc tta 2304  
Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu  
730 735 740 745

gac gaa gca tac gtg atg gct ggt gtg ggc tcc cca tat gtc tcc cgc 2352  
Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg  
750 755 760

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ctt ctg ggc atc tgc ctg aca tcc acg gtg cag ctg gtg aca cag ctt	2400
Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu	
765 770 775	
atg ccc tat ggc tgc ctc tta gac cat gtc cgg gaa aac cgc gga cgc	2448
Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg	
780 785 790	
ctg ggc tcc cag gac ctg ctg aac tgg tgt atg cag att gcc aag ggg	2496
Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly	
795 800 805	
atg agc tac ctg gag gat gtg cgg ctc gta cac agg gac ttg gcc gct	2544
Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala	
810 815 820 825	
cgg aac gtg ctg gtc aag agt ccc aac cat gtc aaa att aca gac ttc	2592
Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe	
830 835 840	
ggg ctg gct cgg ctg ctg gac att gac gag aca gag tac cat gca gat	2640
Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp	
845 850 855	
ggg ggc aag gtg ccc atc aag tgg atg gcg ctg gag tcc att ctc cgc	2688
Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg	
860 865 870	
cgg cgg ttc acc cac cag agt gat gtg tgg agt tat ggt gtg act gtg	2736
Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val	
875 880 885	
tgg gag ctg atg act ttt ggg gcc aaa cct tac gat ggg atc cca gcc	2784
Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala	
890 895 900 905	
cgg gag atc cct gac ctg ctg gaa aag ggg gag cgg ctg ccc cag ccc	2832
Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro	
910 915 920	
ccc atc tgc acc att gat gtc tac atg atc atg gtc aaa tgt tgg atg	2880
Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met	



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925

930

935

att gac tct gaa tgt cgg cca aga ttc cgg gag ttg gtg tct gaa ttc 2928  
Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe  
940 945 950

tcc cgc atg gcc agg gac ccc cag cgc ttt gtg gtc atc cag aat gag 2976  
Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu  
955 960 965

gac ttg ggc cca gcc agt ccc ttg gac agc acc ttc tac cgc tca ctg 3024  
Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser Leu  
970 975 980 985

ctg gag gac gat gac atg ggg gac ctg gtg gat gct gag gag tat ctg 3072  
Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr Leu  
990 995 1000

gta ccc cag cag ggc ttc ttc tgt cca gac cct gcc ccg ggc gct ggg 3120  
Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly Ala Gly  
1005 1010 1015

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Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg Ser Gly Gly  
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ggg gac ctg aca cta ggg ctg gag ccc tct gaa gag gag gcc ccc agg 3216  
Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu Ala Pro Arg  
1035 1040 1045

tct cca ctg gca ccc tcc gaa ggg gct ggc tcc gat gta ttt gat ggt 3264  
Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp Gly  
1050 1055 1060 1065

gac ctg gga atg ggg gca gcc aag ggg ctg caa agc ctc ccc aca cat 3312  
Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu Pro Thr His  
1070 1075 1080

gac ccc agc cct cta cag cgg tac agt gag gac ccc aca gta ccc ctg 3360  
Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro Leu  
1085 1090 1095

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ccc tct gag act gat ggc tac gtt gcc ccc ctg acc tgc agc ccc cag 3408  
 Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro Gln  
 1100 1105 1110

cct gaa tat gtg aac cag cca gat gtt cgg ccc cag ccc cct tcg ccc 3456  
 Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser Pro  
 1115 1120 1125

cga gag ggc cct ctg cct gct gcc cga cct gct ggt gcc act ctg gaa 3504  
 Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu  
 1130 1135 1140 1145

agg gcc aag act ctc tcc cca ggg aag aat ggg gtc gtc aaa gac gtt 3552  
 Arg Ala Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val  
 1150 1155 1160

ttt gcc ttt ggg ggt gcc gtg gag aac ccc gag tac ttg aca ccc cag 3600  
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 1165 1170 1175

gga gga gct gcc cct cag ccc cac cct cct cct gcc ttc agc cca gcc 3648  
 Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala  
 1180 1185 1190

ttc gac aac ctc tat tac tgg gac cag gac cca cca gag cgg ggg gct 3696  
 Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala  
 1195 1200 1205

cca ccc agc acc ttc aaa ggg aca cct acg gca gag aac cca gag tac 3744  
 Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr  
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 Leu Gly Leu Asp Val Pro Val  
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 <212> PRT  
 <213> Homo sapiens

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35 40 45

Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr  
50 55 60

Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val  
65 70 75 80

Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu  
85 90 95

Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr  
100 105 110

Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro  
115 120 125

Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser  
130 135 140

Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln  
145 150 155 160

Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn  
165 170 175

Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys  
180 185 190

His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser  
195 200 205

Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys  
210 215 220

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# BEST AVAILABLE COPY

Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys  
225 230 235 240

Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu  
245 250 255

His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val  
260 265 270

Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg  
275 280 285

Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu  
290 295 300

Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln  
305 310 315 320

Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys  
325 330 335

Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu  
340 345 350

Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys  
355 360 365

Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp  
370 375 380

Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe  
385 390 395 400

Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro  
405 410 415

Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg  
420 425 430

Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu  
435 440 445

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# BEST AVAILABLE COPY

Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly  
450 455 460

Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val  
465 470 475 480

Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr  
485 490 495

Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His  
500 505 510

Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys  
515 520 525

Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys  
530 535 540

Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys  
545 550 555 560

Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys  
565 570 575

Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp  
580 585 590

Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu  
595 600 605

Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln  
610 615 620

Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys  
625 630 635 640

Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Val Ser  
645 650 655

Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly  
660 665 670

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# BEST AVAILABLE COPY

Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg  
675 680 685

Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly  
690 695 700

Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu  
705 710 715 720

Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys  
725 730 735

Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile  
740 745 750

Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu  
755 760 765

Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg  
770 775 780

Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu  
785 790 795 800

Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg  
805 810 815

Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly  
820 825 830

Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala  
835 840 845

Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe  
850 855 860

Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp  
865 870 875 880

Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg  
885 890 895

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# BEST AVAILABLE COPY

Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val  
900 905 910

Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala  
915 920 925

Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro  
930 935 940

Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met  
945 950 955 960

Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe  
965 970 975

Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu  
980 985 990

Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser Leu  
995 1000 1005

Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr Leu  
1010 1015 1020

Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly Ala Gly  
1025 1030 1035 1040

Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg Ser Gly Gly  
1045 1050 1055

Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu Ala Pro Arg  
1060 1065 1070

Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp Gly  
1075 1080 1085

Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu Pro Thr His  
1090 1095 1100

Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro Leu  
1105 1110 1115 1120

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# BEST AVAILABLE COPY

Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro Gln  
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Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser Pro  
 1140 1145 1150

Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu  
 1155 1160 1165

Arg Ala Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val  
 1170 1175 1180

Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln  
 1185 1190 1195 1200

Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala  
 1205 1210 1215

Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala  
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Leu Gly Leu Asp Val Pro Val  
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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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1

5

10

15

gtt ctc tgc ctc caa gcc cag gta act gtt cag tcc tca cct aat ttt 96  
Val Leu Cys Leu Gln Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe  
20 25 30

aca cag cat gtg agg gag cag agc ctg gtg acg gat cag ctc agc cgc 144  
Thr Gln His Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg  
35 40 45

cgc ctc atc cgg acc tac cag ctc tac agc cgc acc agc ggg aag cac 192  
Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His  
50 55 60

gtg cag gtc ctg gcc aac aag cgc atc aac gcc atg gca gaa gac gga 240  
Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly  
65 70 75 80

gac ccc ttc gcg aag ctc att gtg gag acc gat act ttt gga agc aga 288  
Asp Pro Phe Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg  
85 90 95

gtc cga gtt cgc ggc gca gag aca ggt ctc tac atc tgc atg aac aag 336  
Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys  
100 105 110

aag ggg aag cta att gcc aag agc aac ggc aaa ggc aag gac tgc gta 384  
Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val  
115 120 125

ttc aca gag atc gtg ctg gag aac aac tac acg gcg ctg cag aac gcc 432  
Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala  
130 135 140

aag tac gag ggc tgg tac atg gcc ttt acc cgc aag ggc cgg ccc cgc 480  
Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg  
145 150 155 160

aag ggc tcc aag acg cgc cag cat cag cgc gag gtg cac ttc atg aag 528  
Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys  
165 170 175

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cgc ctg ccg cgg ggc cac cac acc acc gag cag agc ctg cgc ttc gag 576  
 Arg Leu Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu  
 180 185 190

ttc ctc aac tac ccg ccc ttc acg cgc agc ctg cgc ggc agc cag agg 624  
 Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg  
 195 200 205

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 Thr Trp Ala Pro Glu Pro Arg  
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 <212> PRT  
 <213> Homo sapiens

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Thr Gln His Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg  
 35 40 45

Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His  
 50 55 60

Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly  
 65 70 75 80

Asp Pro Phe Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg  
 85 90 95

Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys  
 100 105 110

Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val  
 115 120 125

Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala  
 130 135 140

Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg  
 145 150 155 160

Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys  
 165 170 175

Arg Leu Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu  
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Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg  
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Thr Trp Ala Pro Glu Pro Arg  
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<212> DNA

<213> Mus musculus

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<221> CDS

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cgc cag cgc tgg ctc cgt gtt ggg aca ctg gtg ctg gct tta acc gga 96  
 Arg Gln Arg Trp Leu Arg Val Gly Thr Leu Val Leu Ala Leu Thr Gly  
 20 25 30

acc ttc ctc att ggc ttc ctc ttt ggg tgg ttt ata aaa cct tcc aat 144  
 Thr Phe Leu Ile Gly Phe Leu Phe Gly Trp Phe Ile Lys Pro Ser Asn  
 35 40 45

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gaa gct act ggt aat gtt tcc cat tct ggc atg aag aag gag ttt ttg 192  
 Glu Ala Thr Gly Asn Val Ser His Ser Gly Met Lys Lys Glu Phe Leu  
 50 55 60

cat gaa ttg aag gct gag aac atc aaa aaa ttt tta tac aat ttc aca 240  
 His Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr  
 65 70 75 80

cgg aca cca cac ttg gca gga aca caa aat aat ttt gag ctt gca aag 288  
 Arg Thr Pro His Leu Ala Gly Thr Gln Asn Asn Phe Glu Leu Ala Lys  
 85 90 95

caa att cat gac cag tgg aaa gaa ttt ggc ctg gat ttg gtt gag tta 336  
 Gln Ile His Asp Gln Trp Lys Glu Phe Gly Leu Asp Leu Val Glu Leu  
 100 105 110

tcc cat tac gat gtc ttg ctg tcc tat cca aat aaa act cat cct aac 384  
 Ser His Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn  
 115 120 125

tat atc tca ata att aat gaa gat gga aat gag att ttc aaa aca tca 432  
 Tyr Ile Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Lys Thr Ser  
 130 135 140

tta tct gaa cag cca ccc cca gga tat gag aat ata tca gat gta gtg 480  
 Leu Ser Glu Gln Pro Pro Pro Gly Tyr Glu Asn Ile Ser Asp Val Val  
 145 150 155 160

cca cca tac agt gcc ttc tct cca caa ggg aca cca gag ggt gat cta 528  
 Pro Pro Tyr Ser Ala Phe Ser Pro Gln Gly Thr Pro Glu Gly Asp Leu  
 165 170 175

gtg tat gtc aac tat gca cga act gaa gac ttc ttt aaa ctg gaa cgg 576  
 Val Tyr Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg  
 180 185 190

gaa atg aag atc agt tgt tct ggg aag att gtg att gcc aga tat ggg 624  
 Glu Met Lys Ile Ser Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly  
 195 200 205

aaa gtg ttc aga gga aat atg gtt aaa aat gct caa ctg gca ggg gca 672

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210 215 220

aaa gga atg att ctg tac tca gac cct gct gac tac ttt gtt cct gcg 720  
Lys Gly Met Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Val Pro Ala  
225 230 235 240

gtg aag tcc tat cca gat ggc tgg aac ctc cct gga ggt ggt gtc caa 768  
Val Lys Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln  
245 250 255

cgt gga aat gtc tta aat ctt aat ggt gca ggt gac ccg ctc aca cca 816  
Arg Gly Asn Val Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro  
260 265 270

ggt tac cca gca aat gaa cat gct tat agg cat gag ttg aca aac gct 864  
Gly Tyr Pro Ala Asn Glu His Ala Tyr Arg His Glu Leu Thr Asn Ala  
275 280 285

gtt ggc ctt cca agt att cct gtc cat cct att gga tat gat gat gca 912  
Val Gly Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Asp Asp Ala  
290 295 300

cag aaa ctc tta gaa cac atg ggt ggt cca gca ccc cct gac agt agc 960  
Gln Lys Leu Leu Glu His Met Gly Gly Pro Ala Pro Pro Asp Ser Ser  
305 310 315 320

tgg aag gga gga tta aaa gtg cct tac aac gtg gga cct ggc ttt gct 1008  
Trp Lys Gly Gly Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Ala  
325 330 335

gga aac ttt tca aca caa aag gtc aag atg cat att cac tct tac act 1056  
Gly Asn Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser Tyr Thr  
340 345 350

aaa gtg aca aga atc tat aat gtc att ggc acc ctc aaa gga gct ctg 1104  
Lys Val Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Lys Gly Ala Leu  
355 360 365

gaa cca gac aga tat gtt att ctt gga ggt cac cga gac gct tgg gta 1152  
Glu Pro Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ala Trp Val  
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gtg cgg agc ttt gga acc ctg aag aag aaa gga cgg agg cct aga agg	1248
Val Arg Ser Phe Gly Thr Leu Lys Lys Lys Gly Arg Arg Pro Arg Arg	
405 410 415	
aca att ttg ttt gca agc tgg gat gca gaa gaa ttt ggc ctt ctt ggt	1296
Thr Ile Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly	
420 425 430	
tct act gag tgg gca gag gaa cat tca aga ctc cta caa gag cga ggt	1344
Ser Thr Glu Trp Ala Glu Glu His Ser Arg Leu Leu Gln Glu Arg Gly	
435 440 445	
gtg gct tat att aat gct gat tct tcc ata gaa gga aat tac act cta	1392
Val Ala Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu	
450 455 460	
aga gtt gat tgc aca cca ctg atg tac agc tta gtg tac aac cta aca	1440
Arg Val Asp Cys Thr Pro Leu Met Tyr Ser Leu Val Tyr Asn Leu Thr	
465 470 475 480	
aaa gag ctg caa agc cca gat gaa ggt ttt gaa gga aaa tct ctt tat	1488
Lys Glu Leu Gln Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr	
485 490 495	
gac agc tgg aaa gaa aag agt cct tca cct gag ttc att gga atg ccc	1536
Asp Ser Trp Lys Glu Lys Ser Pro Ser Pro Glu Phe Ile Gly Met Pro	
500 505 510	
aga att agc aag ctg ggg tct ggc aat gat ttt gaa gtg ttc ttc caa	1584
Arg Ile Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe Gln	
515 520 525	
aga ctt gga att gct tca ggc aga gcc cga tat act aaa aat tgg aaa	1632
Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn Trp Lys	
530 535 540	
act aac aaa gtc agc agc tat cct ctc tat cac agt gtc tat gaa aca	1680

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Thr Asn Lys Val Ser Ser Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr  
545 550 555 560

tat gag ctg gta gta aaa ttt tat gac cca aca ttt aaa tac cac ctc 1728  
Tyr Glu Leu Val Val Lys Phe Tyr Asp Pro Thr Phe Lys Tyr His Leu  
565 570 575

act gtg gcc cag gtt cga gga gcg atg gta ttt gaa ctt gcc aat tct 1776  
Thr Val Ala Gln Val Arg Gly Ala Met Val Phe Glu Leu Ala Asn Ser  
580 585 590

ata gtg ctt ccc ttt gac tgc caa agt tat gct gta gct ctg aag aag 1824  
Ile Val Leu Pro Phe Asp Cys Gln Ser Tyr Ala Val Ala Leu Lys Lys  
595 600 605

tat gct gac act atc tac aat att tca atg aaa cat cca caa gaa atg 1872  
Tyr Ala Asp Thr Ile Tyr Asn Ile Ser Met Lys His Pro Gln Glu Met  
610 615 620

aag gct tac atg ata tca ttt gat tca ctg ttt tct gca gtc aat aat 1920  
Lys Ala Tyr Met Ile Ser Phe Asp Ser Leu Phe Ser Ala Val Asn Asn  
625 630 635 640

ttt aca gat gtt gca tct aag ttc aat cag aga ctg caa gag tta gac 1968  
Phe Thr Asp Val Ala Ser Lys Phe Asn Gln Arg Leu Gln Glu Leu Asp  
645 650 655

aaa agc aac ccc ata tta ctg aga att atg aat gac cag ctg atg tat 2016  
Lys Ser Asn Pro Ile Leu Leu Arg Ile Met Asn Asp Gln Leu Met Tyr  
660 665 670

ctg gaa cgt gca ttc att gat cct tta ggc tta cca gga agg cct ttc 2064  
Leu Glu Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Gly Arg Pro Phe  
675 680 685

tac agg cat acc atc tat gct cca agc agc cac aac aag tat gca gga 2112  
Tyr Arg His Thr Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly  
690 695 700

gaa tca ttc cct ggg att tat gat gcc ctt ttt gat ata agt agc aaa 2160  
Glu Ser Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Ser Ser Lys  
705 710 715 720

09806703-043001

gtc aat gct tct aag gcc tgg aac gaa gtg aag aga cag att tct att 2208  
 Val Asn Ala Ser Lys Ala Trp Asn Glu Val Lys Arg Gln Ile Ser Ile  
 725 730 735

gca acc ttt aca gtg caa gct gca gca gag act ctg agg gaa gta gct 2256  
 Ala Thr Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Arg Glu Val Ala  
 740 745 750

<210> 8

<211> 752

<212> PRT

<213> Mus musculus

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Arg Gln Arg Trp Leu Arg Val Gly Thr Leu Val Leu Ala Leu Thr Gly  
 20 25 30

Thr Phe Leu Ile Gly Phe Leu Phe Gly Trp Phe Ile Lys Pro Ser Asn  
 35 40 45

Glu Ala Thr Gly Asn Val Ser His Ser Gly Met Lys Lys Glu Phe Leu  
 50 55 60

His Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr  
 65 70 75 80

Arg Thr Pro His Leu Ala Gly Thr Gln Asn Asn Phe Glu Leu Ala Lys  
 85 90 95

Gln Ile His Asp Gln Trp Lys Glu Phe Gly Leu Asp Leu Val Glu Leu  
 100 105 110

Ser His Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn  
 115 120 125

Tyr Ile Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Lys Thr Ser  
 130 135 140



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Leu Ser Glu Gln Pro Pro Pro Gly Tyr Glu Asn Ile Ser Asp Val Val  
145 150 155 160

Pro Pro Tyr Ser Ala Phe Ser Pro Gln Gly Thr Pro Glu Gly Asp Leu  
165 170 175

Val Tyr Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg  
180 185 190

Glu Met Lys Ile Ser Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly  
195 200 205

Lys Val Phe Arg Gly Asn Met Val Lys Asn Ala Gln Leu Ala Gly Ala  
210 215 220

Lys Gly Met Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Val Pro Ala  
225 230 235 240

Val Lys Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln  
245 250 255

Arg Gly Asn Val Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro  
260 265 270

Gly Tyr Pro Ala Asn Glu His Ala Tyr Arg His Glu Leu Thr Asn Ala  
275 280 285

Val Gly Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Asp Asp Ala  
290 295 300

Gln Lys Leu Leu Glu His Met Gly Gly Pro Ala Pro Pro Asp Ser Ser  
305 310 315 320

Trp Lys Gly Gly Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Ala  
325 330 335

Gly Asn Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser Tyr Thr  
340 345 350

Lys Val Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Lys Gly Ala Leu  
355 360 365

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Glu Pro Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ala Trp Val  
370 375 380

Phe Gly Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Ile  
385 390 395 400

Val Arg Ser Phe Gly Thr Leu Lys Lys Lys Gly Arg Arg Pro Arg Arg  
405 410 415

Thr Ile Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly  
420 425 430

Ser Thr Glu Trp Ala Glu Glu His Ser Arg Leu Leu Gln Glu Arg Gly  
435 440 445

Val Ala Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu  
450 455 460

Arg Val Asp Cys Thr Pro Leu Met Tyr Ser Leu Val Tyr Asn Leu Thr  
465 470 475 480

Lys Glu Leu Gln Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr  
485 490 495

Asp Ser Trp Lys Glu Lys Ser Pro Ser Pro Glu Phe Ile Gly Met Pro  
500 505 510

Arg Ile Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe Gln  
515 520 525

Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn Trp Lys  
530 535 540

Thr Asn Lys Val Ser Ser Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr  
545 550 555 560

Tyr Glu Leu Val Val Lys Phe Tyr Asp Pro Thr Phe Lys Tyr His Leu  
565 570 575

Thr Val Ala Gln Val Arg Gly Ala Met Val Phe Glu Leu Ala Asn Ser  
580 585 590

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Ile Val Leu Pro Phe Asp Cys Gln Ser Tyr Ala Val Ala Leu Lys Lys  
 595 600 605

Tyr Ala Asp Thr Ile Tyr Asn Ile Ser Met Lys His Pro Gln Glu Met  
 610 615 620

Lys Ala Tyr Met Ile Ser Phe Asp Ser Leu Phe Ser Ala Val Asn Asn  
 625 630 635 640

Phe Thr Asp Val Ala Ser Lys Phe Asn Gln Arg Leu Gln Glu Leu Asp  
 645 650 655

Lys Ser Asn Pro Ile Leu Leu Arg Ile Met Asn Asp Gln Leu Met Tyr  
 660 665 670

Leu Glu Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Gly Arg Pro Phe  
 675 680 685

Tyr Arg His Thr Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly  
 690 695 700

Glu Ser Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Ser Ser Lys  
 705 710 715 720

Val Asn Ala Ser Lys Ala Trp Asn Glu Val Lys Arg Gln Ile Ser Ile  
 725 730 735

Ala Thr Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Arg Glu Val Ala  
 740 745 750

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 <211> 2082  
 <212> DNA  
 <213> Mus musculus  
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 <222> (1)..(2082)  
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Met Lys Lys Glu Phe Leu His Glu Leu Lys Ala Glu Asn Ile Lys Lys	
1 5 10 15	
ttt tta tac aat ttc aca cgg aca cca cac ttg gca gga aca caa aat	96
Phe Leu Tyr Asn Phe Thr Arg Thr Pro His Leu Ala Gly Thr Gln Asn	
20 25 30	
aat ttt gag ctt gca aag caa att cat gac cag tgg aaa gaa ttt ggc	144
Asn Phe Glu Leu Ala Lys Gln Ile His Asp Gln Trp Lys Glu Phe Gly	
35 40 45	
ctg gat ttg gtt gag tta tcc cat tac gat gtc ttg ctg tcc tat cca	192
Leu Asp Leu Val Glu Leu Ser His Tyr Asp Val Leu Leu Ser Tyr Pro	
50 55 60	
aat aaa act cat cct aac tat atc tca ata att aat gaa gat gga aat	240
Asn Lys Thr His Pro Asn Tyr Ile Ser Ile Ile Asn Glu Asp Gly Asn	
65 70 75 80	
gag att ttc aaa aca tca tta tct gaa cag cca ccc cca gga tat gag	288
Glu Ile Phe Lys Thr Ser Leu Ser Glu Gln Pro Pro Pro Gly Tyr Glu	
85 90 95	
aat ata tca gat gta gtg cca cca tac agt gcc ttc tct cca caa ggg	336
Asn Ile Ser Asp Val Val Pro Pro Tyr Ser Ala Phe Ser Pro Gln Gly	
100 105 110	
aca cca gag ggt gat cta gtg tat gtc aac tat gca cga act gaa gac	384
Thr Pro Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala Arg Thr Glu Asp	
115 120 125	
ttc ttt aaa ctg gaa cgg gaa atg aag atc agt tgt tct ggg aag att	432
Phe Phe Lys Leu Glu Arg Glu Met Lys Ile Ser Cys Ser Gly Lys Ile	
130 135 140	
gtg att gcc aga tat ggg aaa gtg ttc aga gga aat atg gtt aaa aat	480
Val Ile Ala Arg Tyr Gly Lys Val Phe Arg Gly Asn Met Val Lys Asn	
145 150 155 160	
gct caa ctg gca ggg gca aaa gga atg att ctg tac tca gac cct gct	528
Ala Gln Leu Ala Gly Ala Lys Gly Met Ile Leu Tyr Ser Asp Pro Ala	

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165

170

175

gac tac ttt gtt cct gcg gtg aag tcc tat cca gat ggc tgg aac ctc 576  
Asp Tyr Phe Val Pro Ala Val Lys Ser Tyr Pro Asp Gly Trp Asn Leu  
180 185 190

cct gga ggt ggt gtc caa cgt gga aat gtc tta aat ctt aat ggt gca 624  
Pro Gly Gly Gly Val Gln Arg Gly Asn Val Leu Asn Leu Asn Gly Ala  
195 200 205

ggt gac ccg ctc aca cca ggt tac cca gca aat gaa cat gct tat agg 672  
Gly Asp Pro Leu Thr Pro Gly Tyr Pro Ala Asn Glu His Ala Tyr Arg  
210 215 220

cat gag ttg aca aac gct gtt ggc ctt cca agt att cct gtc cat cct 720  
His Glu Leu Thr Asn Ala Val Gly Leu Pro Ser Ile Pro Val His Pro  
225 230 235 240

att gga tat gat gat gca cag aaa ctc tta gaa cac atg ggt ggt cca 768  
Ile Gly Tyr Asp Asp Ala Gln Lys Leu Leu Glu His Met Gly Gly Pro  
245 250 255

gca ccc cct gac agt agc tgg aag gga gga tta aaa gtg cct tac aac 816  
Ala Pro Pro Asp Ser Ser Trp Lys Gly Gly Leu Lys Val Pro Tyr Asn  
260 265 270

gtg gga cct ggc ttt gct gga aac ttt tca aca caa aag gtc aag atg 864  
Val Gly Pro Gly Phe Ala Gly Asn Phe Ser Thr Gln Lys Val Lys Met  
275 280 285

cat att cac tct tac act aaa gtg aca aga atc tat aat gtc att ggc 912  
His Ile His Ser Tyr Thr Lys Val Thr Arg Ile Tyr Asn Val Ile Gly  
290 295 300

acc ctc aaa gga gct ctg gaa cca gac aga tat gtt att ctt gga ggt 960  
Thr Leu Lys Gly Ala Leu Glu Pro Asp Arg Tyr Val Ile Leu Gly Gly  
305 310 315 320

cac cga gac gct tgg gta ttt ggt ggc att gac cct cag agt gga gca 1008  
His Arg Asp Ala Trp Val Phe Gly Gly Ile Asp Pro Gln Ser Gly Ala  
325 330 335

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gct gtt gtt cat gaa att gtg cgg agc ttt gga acc ctg aag aag aaa	1056
Ala Val Val His Glu Ile Val Arg Ser Phe Gly Thr Leu Lys Lys Lys	
340 345 350	
gga cgg agg cct aga agg aca att ttg ttt gca agc tgg gat gca gaa	1104
Gly Arg Arg Pro Arg Arg Thr Ile Leu Phe Ala Ser Trp Asp Ala Glu	
355 360 365	
gaa ttt ggc ctt ctt ggt tct act gag tgg gca gag gaa cat tca aga	1152
Glu Phe Gly Leu Leu Gly Ser Thr Glu Trp Ala Glu Glu His Ser Arg	
370 375 380	
ctc cta caa gag cga ggt gtg gct tat att aat gct gat tct tcc ata	1200
Leu Leu Gln Glu Arg Gly Val Ala Tyr Ile Asn Ala Asp Ser Ser Ile	
385 390 395 400	
gaa gga aat tac act cta aga gtt gat tgc aca cca ctg atg tac agc	1248
Glu Gly Asn Tyr Thr Leu Arg Val Asp Cys Thr Pro Leu Met Tyr Ser	
405 410 415	
tta gtg tac aac cta aca aaa gag ctg caa agc cca gat gaa ggt ttt	1296
Leu Val Tyr Asn Leu Thr Lys Glu Leu Gln Ser Pro Asp Glu Gly Phe	
420 425 430	
gaa gga aaa tct ctt tat gac agc tgg aaa gaa aag agt cct tca cct	1344
Glu Gly Lys Ser Leu Tyr Asp Ser Trp Lys Glu Lys Ser Pro Ser Pro	
435 440 445	
gag ttc att gga atg ccc aga att agc aag ctg ggg tct ggc aat gat	1392
Glu Phe Ile Gly Met Pro Arg Ile Ser Lys Leu Gly Ser Gly Asn Asp	
450 455 460	
ttt gaa gtg ttc ttc caa aga ctt gga att gct tca ggc aga gcc cga	1440
Phe Glu Val Phe Phe Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg	
465 470 475 480	
tat act aaa aat tgg aaa act aac aaa gtc agc agc tat cct ctc tat	1488
Tyr Thr Lys Asn Trp Lys Thr Asn Lys Val Ser Ser Tyr Pro Leu Tyr	
485 490 495	
cac agt gtc tat gaa aca tat gag ctg gta gta aaa ttt tat gac cca	1536
His Ser Val Tyr Glu Thr Tyr Glu Leu Val Val Lys Phe Tyr Asp Pro	

500

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510

aca ttt aaa tac cac ctc act gtg gcc cag gtt cga gga gcg atg gta 1584  
 Thr Phe Lys Tyr His Leu Thr Val Ala Gln Val Arg Gly Ala Met Val  
 515 520 525

ttt gaa ctt gcc aat tct ata gtg ctt ccc ttt gac tgc caa agt tat 1632  
 Phe Glu Leu Ala Asn Ser Ile Val Leu Pro Phe Asp Cys Gln Ser Tyr  
 530 535 540

gct gta gct ctg aag aag tat gct gac act atc tac aat att tca atg 1680  
 Ala Val Ala Leu Lys Lys Tyr Ala Asp Thr Ile Tyr Asn Ile Ser Met  
 545 550 555 560

aaa cat cca caa gaa atg aag gct tac atg ata tca ttt gat tca ctg 1728  
 Lys His Pro Gln Glu Met Lys Ala Tyr Met Ile Ser Phe Asp Ser Leu  
 565 570 575

ttt tct gca gtc aat aat ttt aca gat gtt gca tct aag ttc aat cag 1776  
 Phe Ser Ala Val Asn Asn Phe Thr Asp Val Ala Ser Lys Phe Asn Gln  
 580 585 590

aga ctg caa gag tta gac aaa agc aac ccc ata tta ctg aga att atg 1824  
 Arg Leu Gln Glu Leu Asp Lys Ser Asn Pro Ile Leu Leu Arg Ile Met  
 595 600 605

aat gac cag ctg atg tat ctg gaa cgt gca ttc att gat cct tta ggc 1872  
 Asn Asp Gln Leu Met Tyr Leu Glu Arg Ala Phe Ile Asp Pro Leu Gly  
 610 615 620

tta cca gga agg cct ttc tac agg cat acc atc tat gct cca agc agc 1920  
 Leu Pro Gly Arg Pro Phe Tyr Arg His Thr Ile Tyr Ala Pro Ser Ser  
 625 630 635 640

cac aac aag tat gca gga gaa tca ttc cct ggg att tat gat gcc ctt 1968  
 His Asn Lys Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Leu  
 645 650 655

ttt gat ata agt agc aaa gtc aat gct tct aag gcc tgg aac gaa gtg 2016  
 Phe Asp Ile Ser Ser Lys Val Asn Ala Ser Lys Ala Trp Asn Glu Val  
 660 665 670

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aag aga cag att tct att gca acc ttt aca gtg caa gct gca gca gag 2064  
 Lys Arg Gln Ile Ser Ile Ala Thr Phe Thr Val Gln Ala Ala Ala Glu  
 675 680 685

act ctg agg gaa gta gct 2082  
 Thr Leu Arg Glu Val Ala  
 690

<210> 10

<211> 694

<212> PRT

<213> Mus musculus

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<400> 10

Met Lys Lys Glu Phe Leu His Glu Leu Lys Ala Glu Asn Ile Lys Lys  
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Phe Leu Tyr Asn Phe Thr Arg Thr Pro His Leu Ala Gly Thr Gln Asn  
 20 25 30

Asn Phe Glu Leu Ala Lys Gln Ile His Asp Gln Trp Lys Glu Phe Gly  
 35 40 45

Leu Asp Leu Val Glu Leu Ser His Tyr Asp Val Leu Leu Ser Tyr Pro  
 50 55 60

Asn Lys Thr His Pro Asn Tyr Ile Ser Ile Ile Asn Glu Asp Gly Asn  
 65 70 75 80

Glu Ile Phe Lys Thr Ser Leu Ser Glu Gln Pro Pro Pro Gly Tyr Glu  
 85 90 95

Asn Ile Ser Asp Val Val Pro Pro Tyr Ser Ala Phe Ser Pro Gln Gly  
 100 105 110

Thr Pro Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala Arg Thr Glu Asp  
 115 120 125

Phe Phe Lys Leu Glu Arg Glu Met Lys Ile Ser Cys Ser Gly Lys Ile  
 130 135 140

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Val Ile Ala Arg Tyr Gly Lys Val Phe Arg Gly Asn Met Val Lys Asn  
145 150 155 160

Ala Gln Leu Ala Gly Ala Lys Gly Met Ile Leu Tyr Ser Asp Pro Ala  
165 170 175

Asp Tyr Phe Val Pro Ala Val Lys Ser Tyr Pro Asp Gly Trp Asn Leu  
180 185 190

Pro Gly Gly Gly Val Gln Arg Gly Asn Val Leu Asn Leu Asn Gly Ala  
195 200 205

Gly Asp Pro Leu Thr Pro Gly Tyr Pro Ala Asn Glu His Ala Tyr Arg  
210 215 220

His Glu Leu Thr Asn Ala Val Gly Leu Pro Ser Ile Pro Val His Pro  
225 230 235 240

Ile Gly Tyr Asp Asp Ala Gln Lys Leu Leu Glu His Met Gly Gly Pro  
245 250 255

Ala Pro Pro Asp Ser Ser Trp Lys Gly Gly Leu Lys Val Pro Tyr Asn  
260 265 270

Val Gly Pro Gly Phe Ala Gly Asn Phe Ser Thr Gln Lys Val Lys Met  
275 280 285

His Ile His Ser Tyr Thr Lys Val Thr Arg Ile Tyr Asn Val Ile Gly  
290 295 300

Thr Leu Lys Gly Ala Leu Glu Pro Asp Arg Tyr Val Ile Leu Gly Gly  
305 310 315 320

His Arg Asp Ala Trp Val Phe Gly Gly Ile Asp Pro Gln Ser Gly Ala  
325 330 335

Ala Val Val His Glu Ile Val Arg Ser Phe Gly Thr Leu Lys Lys Lys  
340 345 350

Gly Arg Arg Pro Arg Arg Thr Ile Leu Phe Ala Ser Trp Asp Ala Glu  
355 360 365

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Glu Phe Gly Leu Leu Gly Ser Thr Glu Trp Ala Glu Glu His Ser Arg  
370 375 380

Leu Leu Gln Glu Arg Gly Val Ala Tyr Ile Asn Ala Asp Ser Ser Ile  
385 390 395 400

Glu Gly Asn Tyr Thr Leu Arg Val Asp Cys Thr Pro Leu Met Tyr Ser  
405 410 415

Leu Val Tyr Asn Leu Thr Lys Glu Leu Gln Ser Pro Asp Glu Gly Phe  
420 425 430

Glu Gly Lys Ser Leu Tyr Asp Ser Trp Lys Glu Lys Ser Pro Ser Pro  
435 440 445

Glu Phe Ile Gly Met Pro Arg Ile Ser Lys Leu Gly Ser Gly Asn Asp  
450 455 460

Phe Glu Val Phe Phe Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg  
465 470 475 480

Tyr Thr Lys Asn Trp Lys Thr Asn Lys Val Ser Ser Tyr Pro Leu Tyr  
485 490 495

His Ser Val Tyr Glu Thr Tyr Glu Leu Val Val Lys Phe Tyr Asp Pro  
500 505 510

Thr Phe Lys Tyr His Leu Thr Val Ala Gln Val Arg Gly Ala Met Val  
515 520 525

Phe Glu Leu Ala Asn Ser Ile Val Leu Pro Phe Asp Cys Gln Ser Tyr  
530 535 540

Ala Val Ala Leu Lys Lys Tyr Ala Asp Thr Ile Tyr Asn Ile Ser Met  
545 550 555 560

Lys His Pro Gln Glu Met Lys Ala Tyr Met Ile Ser Phe Asp Ser Leu  
565 570 575

Phe Ser Ala Val Asn Asn Phe Thr Asp Val Ala Ser Lys Phe Asn Gln  
580 585 590

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Arg Leu Gln Glu Leu Asp Lys Ser Asn Pro Ile Leu Leu Arg Ile Met  
 595 600 605

Asn Asp Gln Leu Met Tyr Leu Glu Arg Ala Phe Ile Asp Pro Leu Gly  
 610 615 620

Leu Pro Gly Arg Pro Phe Tyr Arg His Thr Ile Tyr Ala Pro Ser Ser  
 625 630 635 640

His Asn Lys Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Leu  
 645 650 655

Phe Asp Ile Ser Ser Lys Val Asn Ala Ser Lys Ala Trp Asn Glu Val  
 660 665 670

Lys Arg Gln Ile Ser Ile Ala Thr Phe Thr Val Gln Ala Ala Ala Glu  
 675 680 685

Thr Leu Arg Glu Val Ala  
 690

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 <212> DNA  
 <213> Clostridium tetani

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 <222> (1)..(45)

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<210> 12  
 <211> 15  
 <212> PRT  
 <213> Clostridium tetani

<400> 12

Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu  
1 5 10 15

<210> 13

<211> 63

<212> DNA

<213> Clostridium tetani

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<221> CDS

<222> (1)..(63)

<400> 13

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Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser  
1 5 10 15

gct agc cac ctg gaa 63  
Ala Ser His Leu Glu  
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<210> 14

<211> 21

<212> PRT

<213> Clostridium tetani

<400> 14

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser  
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Ala Ser His Leu Glu  
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<210> 15

<211> 25

<212> PRT

<213> Artificial Sequence

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<220>

<223> Description of Artificial Sequence: Fusion of  
tetanus toxoid epitope and PSM

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Gln Glu Arg Gly Val Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly  
1 5 10 15

Ile Thr Glu Leu Arg Val Asp Cys Thr  
20 25

<210> 16

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion of  
tetanus toxoid epitope and PSM

<400> 16

Ala Val Val Leu Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly  
1 5 10 15

Ile Thr Glu Leu Glu Met Lys Thr Tyr  
20 25

<210> 17

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion of  
tetanus toxoid epitope and PSM

<400> 17

Met Phe Leu Glu Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly  
1 5 10 15

Ile Thr Glu Leu His Val Ile Tyr Ala  
20 25

**BEST AVAILABLE COPY**

<210> 18

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion of  
tetanus toxoid epitope and PSM

<400> 18

Asn Ser Arg Leu Leu Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg  
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Val Pro Lys Val Ser Ala Ser His Leu Glu Val Asp Cys Thr Pro  
20 25 30

<210> 19

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion of  
tetanus toxoid epitope and PSM

<400> 19

Val Val Leu Arg Lys Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg  
1 5 10 15

Val Pro Lys Val Ser Ala Ser His Leu Glu Ser Phe Asp Ser Leu

20

25

30

&lt;210&gt; 20

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

**BEST AVAILABLE COPY**

&lt;220&gt;

<223> Description of Artificial Sequence: Fusion of  
tetanus toxoid epitope and PSM

&lt;400&gt; 20

Leu	Met	Phe	Leu	Glu	Phe	Asn	Asn	Phe	Thr	Val	Ser	Phe	Trp	Leu	Arg
1				5					10					15	

Val	Pro	Lys	Val	Ser	Ala	Ser	His	Leu	Glu	Pro	Ser	Ser	His	Asn
			20					25					30	

&lt;210&gt; 21

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Artificial His  
tag

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(18)

&lt;400&gt; 21

cat	cat	cat	cat	cat	cat
His	His	His	His	His	His
1				5	

18

&lt;210&gt; 22

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<211> 6  
<212> PRT  
<213> Artificial Sequence  
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tag

<400> 22  
His His His His His His  
1 5

<210> 23  
<211> 42  
<212> DNA  
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<220>  
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Met Lys His Gln His Gln His Gln His Gln His Gln His Gln  
1 5 10

42

<210> 24  
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tag

<400> 24  
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln  
1 5 10

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<210> 25  
 <211> 69  
 <212> DNA  
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<220>  
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 <222> (1)..(69)

<400> 25  
 atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg ctg ctg tgt gga 48  
 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly  
 1 5 10 15

gca gtc ttc gtt tcg ccc agc 69  
 Ala Val Phe Val Ser Pro Ser  
 20

<210> 26  
 <211> 23  
 <212> PRT  
 <213> Mus musculus

<400> 26  
 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly  
 1 5 10 15

Ala Val Phe Val Ser Pro Ser  
 20

<210> 27  
 <211> 33  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS

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<222> (1)..(33)

<400> 27

gaa caa aaa ctc atc tca gaa gag gat ctg aat

33

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn

1

5

10

<210> 28

<211> 11

<212> PRT

<213> Homo sapiens

<400> 28

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn

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5

10

<210> 29

<211> 75

<212> DNA

<213> Homo sapiens

<220>

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<222> (1)..(75)

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48

Met Lys Asp Ser Cys Ile Thr Val Met Ala Met Ala Leu Leu Ser Gly

1

5

10

15

ttc ttt ttc ttc gcg cgc gcc tcg agc

75

Phe Phe Phe Phe Ala Pro Ala Ser Ser

20

25

<210> 30

<211> 25

<212> PRT

<213> Homo sapiens

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<400> 30

Met Lys Asp Ser Cys Ile Thr Val Met Ala Met Ala Leu Leu Ser Gly  
1 5 10 15

Phe Phe Phe Phe Ala Pro Ala Ser Ser  
20 25

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<210> 31

<211> 60

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(60)

<400> 31

atg aga agg atg ctt ctg cac ttg agt gtt ctg act ctc agc tgt gtc 48  
Met Arg Arg Met Leu Leu His Leu Ser Val Leu Thr Leu Ser Cys Val  
1 5 10 15

tgg gcc act gcc 60  
Trp Ala Thr Ala  
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<210> 32

<211> 20

<212> PRT

<213> Mus musculus

<400> 32

Met Arg Arg Met Leu Leu His Leu Ser Val Leu Thr Leu Ser Cys Val  
1 5 10 15

Trp Ala Thr Ala  
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<210> 33

<211> 20

<212> PRT

<213> Homo sapiens

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<400> 33

Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala

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5

10

15

Pro Asp Thr Arg

20

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